(b) detecting, as in step (a) the level of expression of the nucleic acid sequence in a control sample of tissue cells of the same cell type that do not exhibit uncontrolled growth; and

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(c) comparing the expression level of the nucleic acid sequence in the test cells with the expression level in the control cells, wherein a higher expression level in the test sample indicates the presence of tumor in the mammal.

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25. The method of claim 1 wherein the expression level of the nucleic acid sequence in the test sample cells is at least two-fold greater than in the control cells.

27. The method of claim 26 wherein the cancerous tissue is selected from the group consisting of breast cancer, prostate cancer, colon cancer, squamous cell cancer, small-cell lung cancer, non-small-cell lung cancer, gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer, bladder cancer, hepatoma, colorectal cancer, endometrial carcinoma, salivary gland carcinoma, kidney cancer, vulval cancer, thyroid cancer, and head and neck carcinoma.

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28. A method of diagnosing tumor in a mammal, the method comprising:

(a) detecting the number of copies of nucleic acid sequence in a test sample of tissue cells obtained from the mammal, wherein the cells are suspected of uncontrolled growth and wherein the detecting is by contacting, under high stringency conditions, nucleic acid of the test sample cells with a nucleic acid probe comprising at least 20 contiguous nucleic acid bases from DNA 58125 (SEQ ID NO:1) or its complement (SEQ ID NO:2);

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(b) detecting the number of copies of a nucleic acid marker sequence on the chromosome encoding the nucleic acid sequence in the test sample, which marker gene is not amplified; and

(c) comparing the copy number of the nucleic acid sequence in the test cells with the copy number of the marker sequence, wherein a higher nucleic acid sequence copy number indicates the presence of tumor in the mammal.

29. The method of claim 28 wherein the marker sequence is detected by contacting, under high stringency conditions, nucleic acid of the test sample with a nucleic acid marker sequence comprising at least 20 contiguous nucleic acid bases from a sequence, or its complement, in Chromosome 16 from chromosomal regions selected from the group consisting of regions P7, P55, P89, P90, P92, P93, P94, P95, P99, P154, and P208.

30. The method of claim 29 wherein the marker sequence is selected from the group consisting of Stanford Human Genome Center Marker Probes SHGC-2835, SHGC-9643, SHGC-11302, SHGC-2726, SHGC-36123, SHGC-35326, IB391, GATA7B02, SHGC-33727, and SHGC-13574.

33. The method of claim 26 wherein the nucleic acid sequence copy number in the test sample cells is at least two-fold greater than the copy number of unamplified marker sequences.

35. The method of claim 28 wherein the cancerous tissue is selected from the group consisting of breast cancer, prostate cancer, colon cancer, squamous cell cancer, small-cell lung cancer, non-small-cell lung cancer, gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer, bladder cancer, hepatoma, colorectal cancer, endometrial carcinoma, salivary gland carcinoma, kidney cancer, vulval cancer, thyroid cancer, and head and neck carcinoma.